SEQ SEARCH SUMMARY

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 11:26:05 ; Search time 9284 Seconds
                                         (without alignments)
                                         11115.873 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1:   gb_ba:*
                2:   gb_htg:*
                3:   gb_in:*
                4:   gb_om:*
                5:   gb_ov:*
                6:   gb_pat:*
                7:   gb_ph:*
                8:   gb_pl:*
                9:   gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
                15: em_ba:*
                16: em_fun:*
                17: em_hum:*
                18: em_in:*
                19: em_mu:*
                20: em_om:*
                21: em_or:*
                22: em_ov:*
                23: em_pat:*
                24: em_ph:*
                25: em_pl:*
                26: em_ro:*
                27: em_sts:*

Regular search w/ SEQ ID NO:1

```
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Appl's WO (handwritten)

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	2381	6	AX404864	AX404864 Sequence
2	2377.8	99.9	333150	1	AP005277	AP005277 Corynebac
3	2377.8	99.9	349980	6	AX127146	AX127146 Sequence
4	2377.8	99.9	349980	6	AX127147	AX127147 Sequence
5	2156.8	90.6	2326	6	AX764083	AX764083 Sequence
6	2126.8	89.3	2196	6	AX121362	AX121362 Sequence
7	2126.8	89.3	2196	6	BD163479	BD163479 Novel pol
8	1498.4	62.9	308650	1	AP005218	AP005218 Corynebac
9	1039	43.6	347625	1	BX248356	BX248356 Corynebac
10	590.6	24.8	11785	1	AE012833	AE012833 Chlorobiu
c 11	583.6	24.5	12009	1	AE011922	AE011922 Xanthomon
c 12	574.2	24.1	10101	1	AE012376	AE012376 Xanthomon
13	563.8	23.7	17916	1	AE007004	AE007004 Mycobacte
14	563.8	23.7	75216	6	AX704275	AX704275 Sequence
15	563.8	23.7	348264	1	BX842576	BX842576 Mycobacte
16	562.2	23.6	299450	1	BX248338	BX248338 Mycobacte
17	545	22.9	2333	1	KPNDEAD	L08387 Klebsiella
c 18	519.8	21.8	300029	1	AE012553	AE012553 Xylella f
c 19	519.6	21.8	12008	1	AE003878	AE003878 Xylella f
c 20	516	21.7	11002	1	AE015331	AE015331 Shigella
c 21	516	21.7	292497	1	AE016989	AE016989 Shigella
c 22	516	21.7	300359	1	AE016767	AE016767 Escherich
c 23	514.6	21.6	14820	1	AE000397	AE000397 Escherich
c 24	514.6	21.6	14820	6	AX370215	AX370215 Sequence
c 25	514.6	21.6	14820	6	AX370260	AX370260 Sequence
c 26	514.6	21.6	110000	1	ECOUW67_0	U18997 Escherichia
c 27	513.6	21.6	110000	2	AC074221_3	Continuation (4 of
c 28	511.4	21.5	20120	1	AE008851	AE008851 Salmonell
c 29	508	21.3	10994	1	AE005544	AE005544 Escherich
c 30	508	21.3	307962	1	AP002564	AP002564 Escherich
31	500.8	21.0	2863	6	BD103627	BD103627 Method an
c 32	500.2	21.0	258050	1	AL627278	AL627278 Salmonell
c 33	500.2	21.0	301574	1	AE016844	AE016844 Salmonell

Handwritten annotations:
- Row 1: WO 02/26787
- Row 2: 2002 GenBank (AP005277 boxed)
- Row 3: EP 1108790
- Row 4: EP → Pompejus
- Row 5: WO 03/40289
- Row 6: EP
- Row 7: JP 2002191370

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 11:24:21 ; Search time 973 Seconds
                                         (without alignments)
                                         10395.642 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                    %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   2381 100.0   2381   6 AAD28043 *WO 02/26787*   Aad28043 Corynebac
     2 2377.8   99.9 349980   5 AAH68527 *EP 1108790*   Aah68527 C glutami
     3 2377.8   99.9 349980   5 AAH68528 *EP*   Aah68528 C glutami
     4 2126.8   89.3   2196   5 AAH66243 *EP*   Aah66243 C glutami
     5   1674   70.3   1674   7 ACA00444 *DE 10128510*   Aca00444 C. glutam
     6   997.2   41.9   1694   7 ACA29908   Aca29908 Prokaryot
     7   614.8   25.8   1698   7 ACA37563   Aca37563 Prokaryot

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:22:26 ; Search time 195 Seconds
                                      (without alignments)
                                      6776.093 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	563.8	23.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	2	563.8	23.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	3	500.8	21.0	2863	4	US-09-293-427-5	Sequence 5, Appli
	4	475.2	20.0	1455	4	US-09-489-039A-6537	Sequence 6537, Ap
	5	465.4	19.5	2100	4	US-09-252-991A-9660	Sequence 9660, Ap
	6	465.2	19.5	1785	4	US-09-252-991A-9701	Sequence 9701, Ap
c	7	403.6	17.0	1329	4	US-09-489-039A-6439	Sequence 6439, Ap
	8	373	15.7	1851	4	US-09-543-681A-1595	Sequence 1595, Ap
	9	357.6	15.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
	10	357.6	15.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c	11	295.8	12.4	640681	4	US-09-790-988-1	Sequence 1, Appli

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 17:44:52 ; Search time 1060 Seconds
                                           (without alignments)
                                           10208.487 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Nakagawa USPAP 2002 0197605

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	2381	9	US-09-963-790A-1 *Appl.*	Sequence 1, Appli
2	2377.8	99.9	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	2126.8	89.3	2196	9	US-09-738-626-1278	Sequence 1278, Ap
4	997.2	41.9	1694	13	US-10-282-122A-17778	Sequence 17778, A
5	614.8	25.8	1698	13	US-10-282-122A-25433	Sequence 25433, A
6	577.4	24.3	1515	16	US-10-369-493-39349	Sequence 39349, A
7	577.4	24.3	1515	16	US-10-369-493-39740	Sequence 39740, A
8	572.6	24.0	1392	16	US-10-369-493-38983	Sequence 38983, A
9	563.8	23.7	1692	13	US-10-282-122A-28332	Sequence 28332, A
10	563.8	23.7	75216	15	US-10-080-170-646	Sequence 646, App
11	562.2	23.6	1689	13	US-10-282-122A-26634	Sequence 26634, A
12	545	22.9	1929	13	US-10-282-122A-23307	Sequence 23307, A
13	540	22.7	1893	13	US-10-282-122A-20013	Sequence 20013, A
14	523	22.0	1695	16	US-10-369-493-32859	Sequence 32859, A
15	521	21.9	1737	16	US-10-369-493-33102	Sequence 33102, A
16	519.6	21.8	1845	16	US-10-369-493-41191	Sequence 41191, A
17	514.6	21.6	1941	9	US-09-815-242-6214	Sequence 6214, Ap
18	514.6	21.6	1941	13	US-10-282-122A-7172	Sequence 7172, Ap
19	500.2	21.0	1941	9	US-09-815-242-9671	Sequence 9671, Ap
20	500.2	21.0	1941	13	US-10-282-122A-39344	Sequence 39344, A
21	488.8	20.5	1920	16	US-10-369-493-24059	Sequence 24059, A
22	469	19.7	1647	16	US-10-369-493-44595	Sequence 44595, A
23	468.4	19.7	1704	9	US-09-815-242-7788	Sequence 7788, Ap
24	468.4	19.7	1704	13	US-10-282-122A-30236	Sequence 30236, A
25	448.8	18.8	1726	13	US-10-282-122A-33397	Sequence 33397, A
26	446.8	18.8	1708	16	US-10-369-493-37429	Sequence 37429, A
27	445.4	18.7	1714	13	US-10-282-122A-31439	Sequence 31439, A
28	443.2	18.6	1995	13	US-10-282-122A-41749	Sequence 41749, A
29	398.6	16.7	1415	13	US-10-282-122A-36654	Sequence 36654, A
30	367.8	15.4	1833	13	US-10-282-122A-32588	Sequence 32588, A
31	357.6	15.0	1842	9	US-09-815-242-6893	Sequence 6893, Ap
32	357.6	15.0	1842	13	US-10-282-122A-21926	Sequence 21926, A
33	357.6	15.0	1830121	15	US-10-329-960-1	Sequence 1, Appli
34	357.6	15.0	1830121	16	US-10-329-670-1	Sequence 1, Appli
35	355.6	14.9	1992	13	US-10-282-122A-41471	Sequence 41471, A
36	347.6	14.6	1833	13	US-10-282-122A-31003	Sequence 31003, A
37	347.6	14.6	1833	13	US-10-406-686A-87	Sequence 87, Appl
38	337.2	14.2	1337	16	US-10-369-493-42992	Sequence 42992, A
39	328.2	13.8	1620	16	US-10-369-493-31859	Sequence 31859, A
40	326	13.7	1767	13	US-10-282-122A-25322	Sequence 25322, A
41	324.4	13.6	1701	16	US-10-369-493-32830	Sequence 32830, A
c 42	295.8	12.4	640681	9	US-09-790-988-1	Sequence 1, Appli
43	284.4	11.9	1722	13	US-10-282-122A-14689	Sequence 14689, A
44	280.8	11.8	1431	16	US-10-369-493-40518	Sequence 40518, A
45	278.4	11.7	1377	16	US-10-369-493-44540	Sequence 44540, A

ALIGNMENTS

RESULT 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004   Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:30:16 ; Search time 6138 Seconds
                                            (without alignments)
                                            11583.879 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

```
28:  gb_gss1:*
29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	346.8	14.6	1231	29	CG748798	CG748798 P042-4-C0
c	2	324.4	13.6	1269	29	CG747958	CG747958 P041-3-G1
c	3	241	10.1	3539	28	BH770982	BH770982 LLMGtag70
	4	213.2	9.0	1101	28	BZ549647	BZ549647 pacs1-60_
	5	195.4	8.2	1443	12	BM321064	BM321064 rockefell
	6	193.6	8.1	1929	11	AY104966	AY104966 Zea mays
c	7	190.6	8.0	936	28	BZ566692	BZ566692 pacs2-164
	8	190	8.0	1175	14	CD508153	CD508153 CDA89-C04
c	9	183.4	7.7	712	28	BZ549701	BZ549701 pacs1-60_
	10	181.8	7.6	948	28	BZ553880	BZ553880 pacs1-60_
	11	180.2	7.6	1609	11	AY109160	AY109160 Zea mays
	12	177.2	7.4	1772	11	AK077429	AK077429 Mus muscu
	13	172.8	7.3	1393	11	BC032078	BC032078 Homo sapi
	14	172.4	7.2	1793	11	BC012282	BC012282 Mus muscu
	15	172	7.2	1748	11	AK076982	AK076982 Mus muscu
	16	172	7.2	1752	11	AK010310	AK010310 Mus muscu
	17	167.4	7.0	544	28	AQ989915	AQ989915 Rfc00591
	18	167	7.0	1418	11	AK010644	AK010644 Mus muscu
	19	167	7.0	1438	11	AK075920	AK075920 Mus muscu
	20	163.6	6.9	1165	14	CD507904	CD507904 CDA87-G05
	21	163.6	6.9	1201	9	AL568646	AL568646 AL568646
	22	159.8	6.7	935	14	CF651366	CF651366 29-E00921
	23	158.2	6.6	1050	29	AY414350	AY414350 Mus muscu
	24	157	6.6	688	14	CF842193	CF842193 psHB018xI
c	25	156.8	6.6	696	28	BH143507	BH143507 TDGEA79TH
	26	156.4	6.6	907	14	CK263230	CK263230 EST709308
	27	155.6	6.5	786	28	BZ564147	BZ564147 pacs2-164
	28	155.6	6.5	802	13	BU476989	BU476989 603841415
	29	155.2	6.5	972	11	CNS08PRP	BX022817 Single re
	30	153	6.4	1031	11	CNS08DJ2	BX006954 Single re
	31	152.6	6.4	835	28	BZ565507	BZ565507 pacs2-164
	32	152.4	6.4	1091	14	CK206257	CK206257 FGAS01784
	33	152	6.4	1012	13	BU112303	BU112303 603129440
	34	151.2	6.4	1059	29	AY404229	AY404229 Homo sapi
	35	150	6.3	694	14	CF886658	CF886658 tric084xc
	36	150	6.3	748	14	CB907999	CB907999 tric084xc
	37	149.4	6.3	1163	14	CD497898	CD497898 CDA30-E05
	38	148.2	6.2	1201	9	AL535247	AL535247 AL535247
	39	148.2	6.2	2972	11	AK031534	AK031534 Mus muscu
	40	147.6	6.2	871	14	CD439282	CD439282 EL01N0523
	41	147	6.2	1033	11	CNS090JP	BX036785 Single re
	42	146.6	6.2	2986	11	AK028274	AK028274 Mus muscu
	43	146.6	6.2	3956	11	BC043699	BC043699 Mus muscu
	44	146.4	6.1	1629	11	AK076509	AK076509 Mus muscu
	45	145.8	6.1	704	13	BU406237	BU406237 603482292

```
                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         May 26, 2004, 19:30:42 ; Search time 9282 Seconds
                                        (without alignments)
                                        11118.268 Million cell updates/sec


Title:          US-09-963-790A-1
Perfect score:  2381
Sequence:       1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381


Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       3470272 seqs, 21671516995 residues

Word size :     0

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :      GenEmbl:*
                1:  gb_ba:*
                2:  gb_htg:*
                3:  gb_in:*
                4:  gb_om:*
                5:  gb_ov:*
                6:  gb_pat:*
                7:  gb_ph:*
                8:  gb_pl:*
                9:  gb_pr:*
                10:  gb_ro:*
                11:  gb_sts:*
                12:  gb_sy:*
                13:  gb_un:*
                14:  gb_vi:*
                15:  em_ba:*
                16:  em_fun:*
                17:  em_hum:*
                18:  em_in:*
                19:  em_mu:*
                20:  em_om:*
                21:  em_or:*
                22:  em_ov:*
                23:  em_pat:*
                24:  em_ph:*
                25:  em_pl:*
                26:  em_ro:*
                27:  em_sts:*
```

OLIGO Search w/SEQ ID NO:1

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	2381	100.0	2381	6	AX404864	WO 02/26787	AX404864 Sequence
	2	2279	95.7	333150	1	AP005277	2002 GenBank	[AP005277] Corynebac
	3	2279	95.7	349980	6	AX127146	EP 1108790	AX127146 Sequence
	4	2279	95.7	349980	6	AX127147	EP	AX127147 Sequence → Pompejus
	5	2058	86.4	2326	6	AX764083	WO 03/40289	AX764083 Sequence
	6	2028	85.2	2196	6	AX121362	EP	AX121362 Sequence
	7	2028	85.2	2196	6	BD163479	JP 2002191370	BD163479 Novel pol
	8	44	1.8	308650	1	AP005218	2002 GenBank	[AP005218] Corynebac efficiens
c	9	26	1.1	10101	1	AE012376	2002 "	[AE012376] Xanthomon
	10	26	1.1	123385	1	BX640452	2003 "	[BX640452] Bordetell
	11	26	1.1	255260	1	BX640436	2003 "	[BX640436] Bordetell
	12	26	1.1	346359	1	BX640411	2003 "	[BX640411] Bordetell
c	13	26	1.1	347356	1	BX640437	2003 "	[BX640437] Bordetell
	14	26	1.1	347625	1	BX248356	2003 "	[BX248356] Corynebac diptheriae
	15	26	1.1	348134	1	BX640420	2003 "	[BX640420] Bordetell
c	16	26	1.1	348251	1	BX640423		BX640423 Bordetell
	17	24	1.0	12514	1	AE012011		AE012011 Xanthomon
c	18	24	1.0	320150	1	AP005033		AP005033 Streptomy
	19	23	1.0	10491	1	AE005859		AE005859 Caulobact
c	20	23	1.0	12039	1	AE009534		AE009534 Brucella
	21	23	1.0	12080	1	AE014406		AE014406 Brucella
c	22	23	1.0	109911	2	AC118330_4		Continuation (5 of
	23	23	1.0	190050	1	AL646059		AL646059 Ralstonia
c	24	23	1.0	198050	1	AL646061		AL646061 Ralstonia
c	25	23	1.0	217794	2	AC111124		AC111124 Mus muscu
	26	23	1.0	237801	2	AC137306		AC137306 Rattus no
c	27	23	1.0	238039	2	AC137290		AC137290 Rattus no
c	28	23	1.0	300750	1	AP006576		AP006576 Gloeobact
	29	23	1.0	301617	1	AE016911		AE016911 Chromobac
	30	23	1.0	305584	1	AE016920		AE016920 Chromobac
c	31	23	1.0	311000	1	SCO939122		AL939122 Streptomy
	32	23	1.0	311583	2	AC105794		AC105794 Rattus no
	33	23	1.0	347660	1	AP002994		AP002994 Mesorhizo

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 17:48:26 ; Search time 974 Seconds
                                         (without alignments)
                                         10384.969 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.........ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size :   0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   2381   100.0   2381 6 AAD28043 *wo 02/26787*   Aad28043 Corynebac
     2   2279   95.7 349980 5 AAH68527 *EP 1108790*   Aah68527 C glutami
     3   2279   95.7 349980 5 AAH68528 *EP*   Aah68528 C glutami
     4   2028   85.2   2196 5 AAH66243 *EP*   Aah66243 C glutami *PR*
     5   1674   70.3   1674 7 ACA00444 *DE 10128510 (2001)* Aca00444 C. glutam — *June*
     6   184   7.7   273 7 ACA00443   *"*   Aca00443 C. glutam
     7   26   1.1   1694 7 ACA29908 *wo 02/77183*   Aca29908 Prokaryot

GenCore version 5.1.6
Copyright (c) 1993 - 2004   Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 21:48:17 ; Search time 193 Seconds
                                         (without alignments)
                                         6846.311 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	0.8	483	4	US-09-252-991A-5687	Sequence 5687, Ap
2	20	0.8	1284	4	US-09-489-039A-841	Sequence 841, App
3	20	0.8	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
4	20	0.8	2863	4	US-09-293-427-5	Sequence 5, Appli
c 5	20	0.8	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
6	20	0.8	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
7	20	0.8	68750	3	US-09-335-409-1	Sequence 1, Appli
8	20	0.8	68750	4	US-09-568-102-1	Sequence 1, Appli
9	20	0.8	68750	4	US-09-567-969-1	Sequence 1, Appli
10	20	0.8	68750	4	US-09-568-480-1	Sequence 1, Appli
11	20	0.8	68750	4	US-09-568-486-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:22:22 ; Search time 1947 Seconds
                                          (without alignments)
                                          5562.883 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size :   0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2381	100.0	2381	9	US-09-963-790A-1	Sequence 1, Appli
	2	2279	95.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
	3	2028	85.2	2196	9	US-09-738-626-1278	Sequence 1278, Ap
	4	26	1.1	1392	16	US-10-369-493-38983	Sequence 38983, A
	5	26	1.1	1515	16	US-10-369-493-39349	Sequence 39349, A
	6	26	1.1	1515	16	US-10-369-493-39740	Sequence 39740, A
	7	26	1.1	1694	13	US-10-282-122A-17778	Sequence 17778, A
	8	26	1.1	1722	13	US-10-282-122A-14689	Sequence 14689, A
	9	25	1.0	1708	16	US-10-369-493-37429	Sequence 37429, A
	10	24	1.0	2064	15	US-10-156-761-2902	Sequence 2902, Ap
	11	24	1.0	125746	15	US-10-156-761-15102	Sequence 15102, A
c	12	24	1.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
	13	23	1.0	1326	16	US-10-369-493-41631	Sequence 41631, A
	14	23	1.0	1404	16	US-10-369-493-35503	Sequence 35503, A
	15	23	1.0	1554	16	US-10-369-493-40612	Sequence 40612, A
	16	23	1.0	1584	16	US-10-369-493-35498	Sequence 35498, A
	17	22	0.9	198	11	US-09-864-408A-6929	Sequence 6929, Ap
	18	22	0.9	603	15	US-10-156-761-1568	Sequence 1568, Ap
c	19	22	0.9	2742	13	US-10-282-122A-17561	Sequence 17561, A
	20	21	0.9	28	9	US-09-963-790A-3	Sequence 3, Appli
c	21	21	0.9	28	9	US-09-963-790A-4	Sequence 4, Appli
	22	21	0.9	600	16	US-10-369-493-41629	Sequence 41629, A
c	23	20	0.8	503	10	US-09-918-995-34274	Sequence 34274, A
	24	20	0.8	1266	9	US-09-815-242-7606	Sequence 7606, Ap
	25	20	0.8	1335	16	US-10-369-493-35231	Sequence 35231, A
	26	20	0.8	1387	16	US-10-369-493-35268	Sequence 35268, A
c	27	20	0.8	1584	15	US-10-270-333-140	Sequence 140, App
	28	20	0.8	1941	9	US-09-815-242-6214	Sequence 6214, Ap
	29	20	0.8	1941	13	US-10-282-122A-7172	Sequence 7172, Ap
	30	20	0.8	4185	15	US-10-270-333-139	Sequence 139, App
	31	20	0.8	68750	14	US-10-014-717-1	Sequence 1, Appli
	32	20	0.8	71989	13	US-09-727-889-2	Sequence 2, Appli
c	33	20	0.8	203070	13	US-10-087-192-247	Sequence 247, App
	34	19	0.8	480	9	US-09-991-496-132	Sequence 132, App
	35	19	0.8	515	9	US-09-917-800A-583	Sequence 583, App
c	36	19	0.8	520	9	US-09-874-923-29	Sequence 29, Appl
c	37	19	0.8	520	9	US-09-991-496-29	Sequence 29, Appl
	38	19	0.8	522	15	US-10-156-761-2688	Sequence 2688, Ap
	39	19	0.8	528	13	US-10-424-599-47907	Sequence 47907, A
	40	19	0.8	546	15	US-10-156-761-1619	Sequence 1619, Ap
	41	19	0.8	557	9	US-09-917-800A-340	Sequence 340, App
	42	19	0.8	561	15	US-10-156-761-3799	Sequence 3799, Ap
	43	19	0.8	871	13	US-10-424-599-9675	Sequence 9675, Ap
	44	19	0.8	1098	13	US-10-389-647-129	Sequence 129, App
c	45	19	0.8	1137	15	US-10-156-761-6123	Sequence 6123, Ap

ALIGNMENTS

RESULT 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004   Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 21:41:22 ; Search time 6139 Seconds
                                          (without alignments)
                                          11581.992 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga..........ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size :   0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

```
  28:  gb_gss1:*
  29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	1.0	413	14	CK233812	CK233812 re20a03.y
	2	23	1.0	604	14	CF980889	CF980889 re10b06.y
	3	22	0.9	471	9	AU284741	AU284741 AU284741
	4	22	0.9	478	14	CF075999	CF075999 Hd_mx17_6
	5	22	0.9	562	12	BJ411196	BJ411196 BJ411196
	6	22	0.9	631	9	AU268561	AU268561 AU268561
c	7	22	0.9	660	12	BM634053	BM634053 170006688
c	8	22	0.9	714	12	BM656204	BM656204 170006873
c	9	21	0.9	573	13	BU543982	BU543982 GM880001A
	10	21	0.9	575	28	BZ345001	BZ345001 hr43d08.b
	11	21	0.9	606	12	BM603218	BM603218 170006870
	12	21	0.9	612	28	AZ418854	AZ418854 1M0195C09
	13	21	0.9	715	13	BU634805	BU634805 018D02 In
	14	21	0.9	848	10	BF260369	BF260369 HVSMEf002
c	15	20	0.8	160	28	AZ921472	AZ921472 1006030B0
	16	20	0.8	261	14	CD942465	CD942465 RBX_51 Ge
	17	20	0.8	262	14	CD947789	CD947789 SAB_30 Ge
	18	20	0.8	262	14	CD950568	CD950568 SAR_125 G
	19	20	0.8	262	14	CD951995	CD951995 SAZ_86 Ge
	20	20	0.8	263	14	CD948209	CD948209 SAD_64 Ge
c	21	20	0.8	275	12	BI674592	BI674592 949022D11
	22	20	0.8	305	9	AA571940	AA571940 vg12d02.r
c	23	20	0.8	327	28	BH228484	BH228484 1006147C0
c	24	20	0.8	330	28	BH228575	BH228575 1006147F0
c	25	20	0.8	340	28	BH217878	BH217878 1006060G0
	26	20	0.8	344	13	BQ760997	BQ760997 EBro04_SQ
c	27	20	0.8	344	28	BH216414	BH216414 1006042E0
c	28	20	0.8	351	28	BH217881	BH217881 1006060G0
c	29	20	0.8	352	28	AZ921694	AZ921694 1006031E0
c	30	20	0.8	352	28	BH216419	BH216419 1006042E0
c	31	20	0.8	352	28	BH228573	BH228573 1006147F0
c	32	20	0.8	353	28	BH228482	BH228482 1006147C0
c	33	20	0.8	355	28	BH228632	BH228632 1006147H0
	34	20	0.8	363	13	BQ993892	BQ993892 QGF5M01.y
	35	20	0.8	383	10	AW417369	AW417369 53455 MAR
	36	20	0.8	385	10	AW115311	AW115311 rs65e07.y
	37	20	0.8	393	10	AW307746	AW307746 1617 MARC
c	38	20	0.8	399	14	CF629810	CF629810 zmrws48_0
	39	20	0.8	404	14	CD947936	CD947936 SAC_212_G
	40	20	0.8	410	12	BI336407	BI336407 AR095H07S
	41	20	0.8	462	14	CF215031	CF215031 CAST0001_
c	42	20	0.8	471	14	CF215115	CF215115 CAST0001_
c	43	20	0.8	472	29	CG340791	CG340791 OGVCR31TH
	44	20	0.8	482	10	BE481452	BE481452 166898 BA
	45	20	0.8	484	12	BM106031	BM106031 509650 MA